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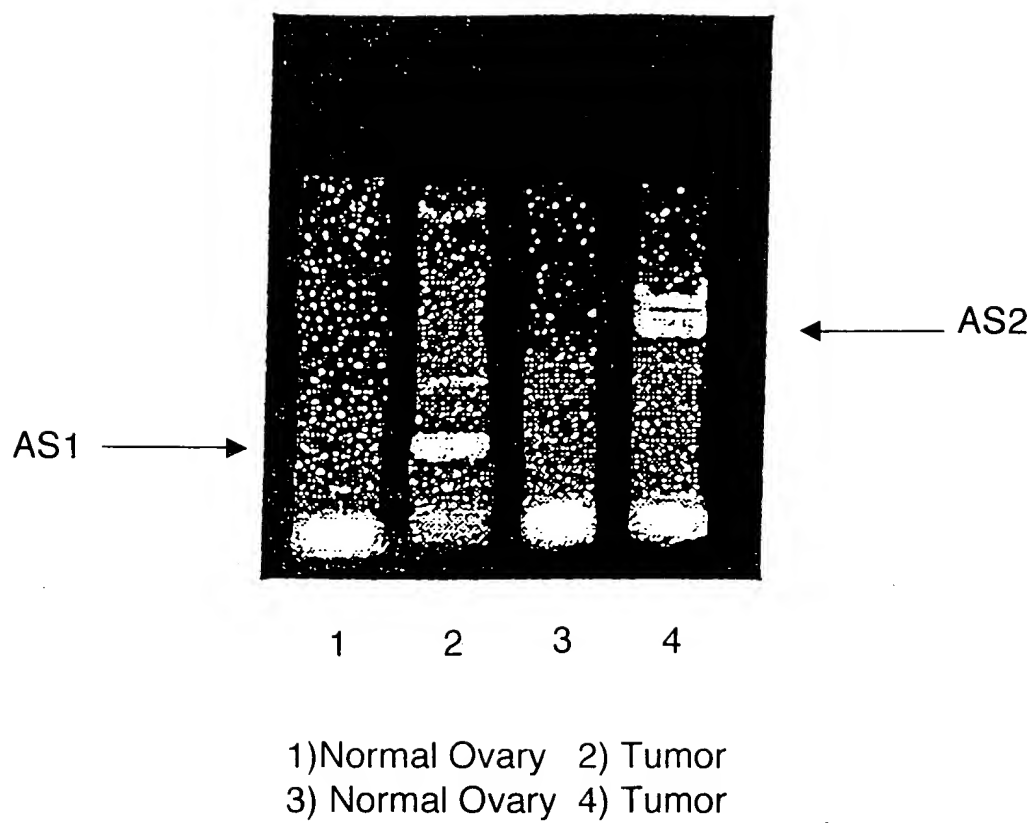


Fig. 1

[illegible]

Fig. 2

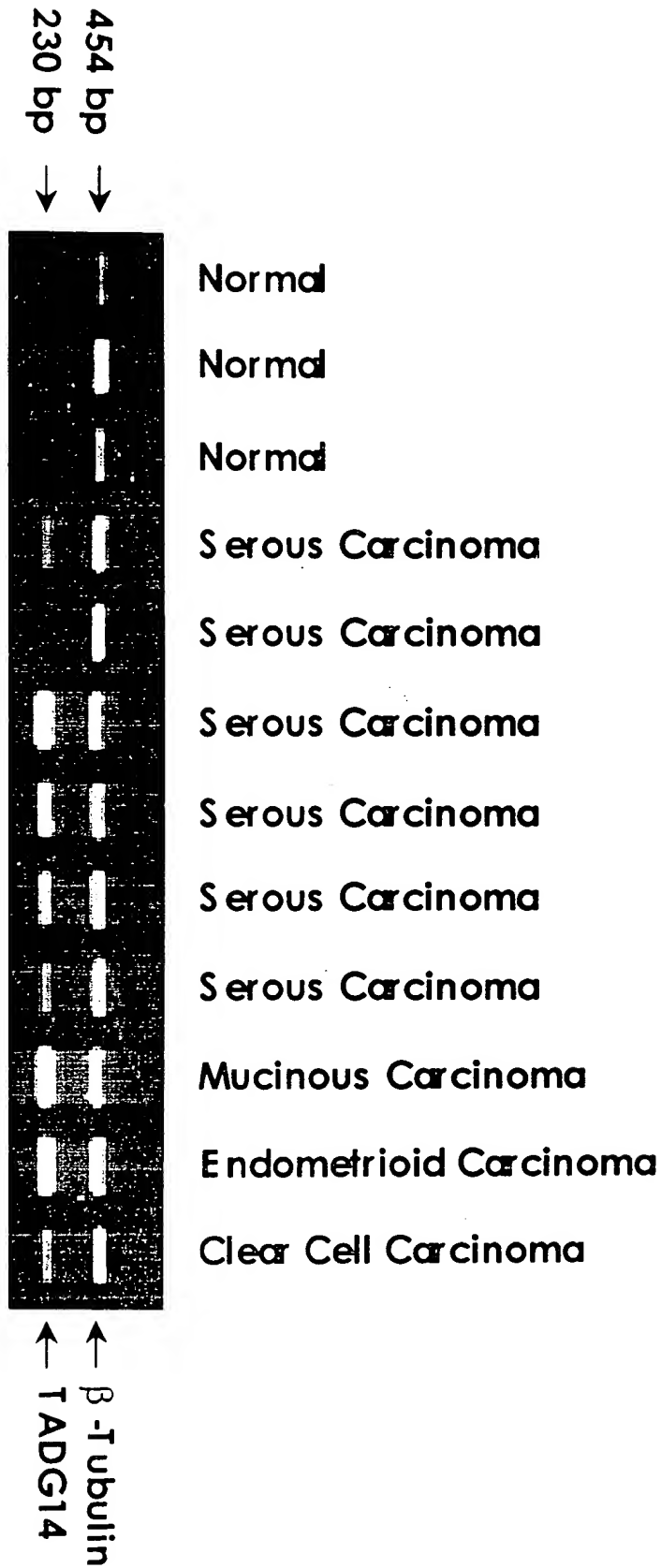


Fig. 3

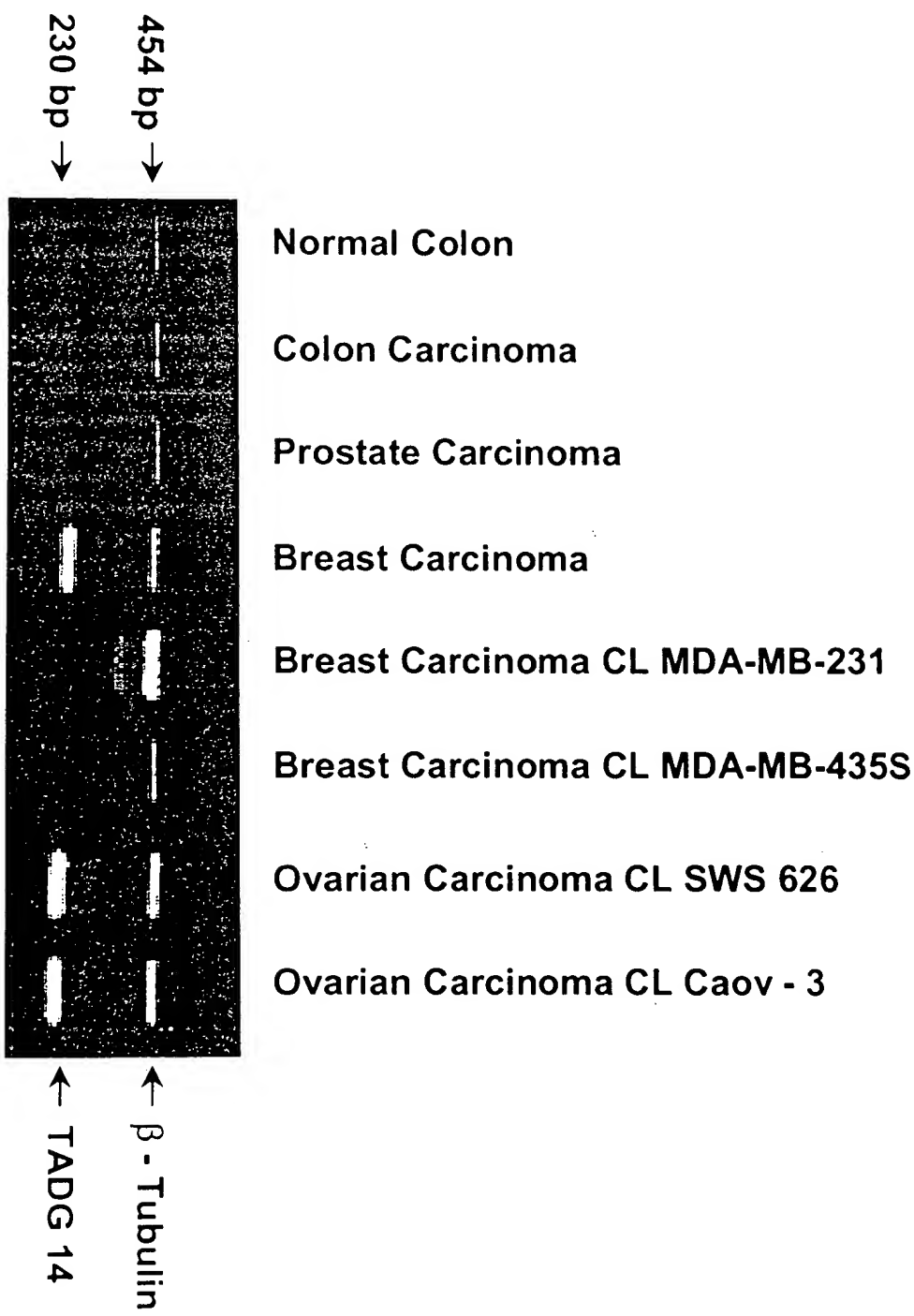


Fig. 4

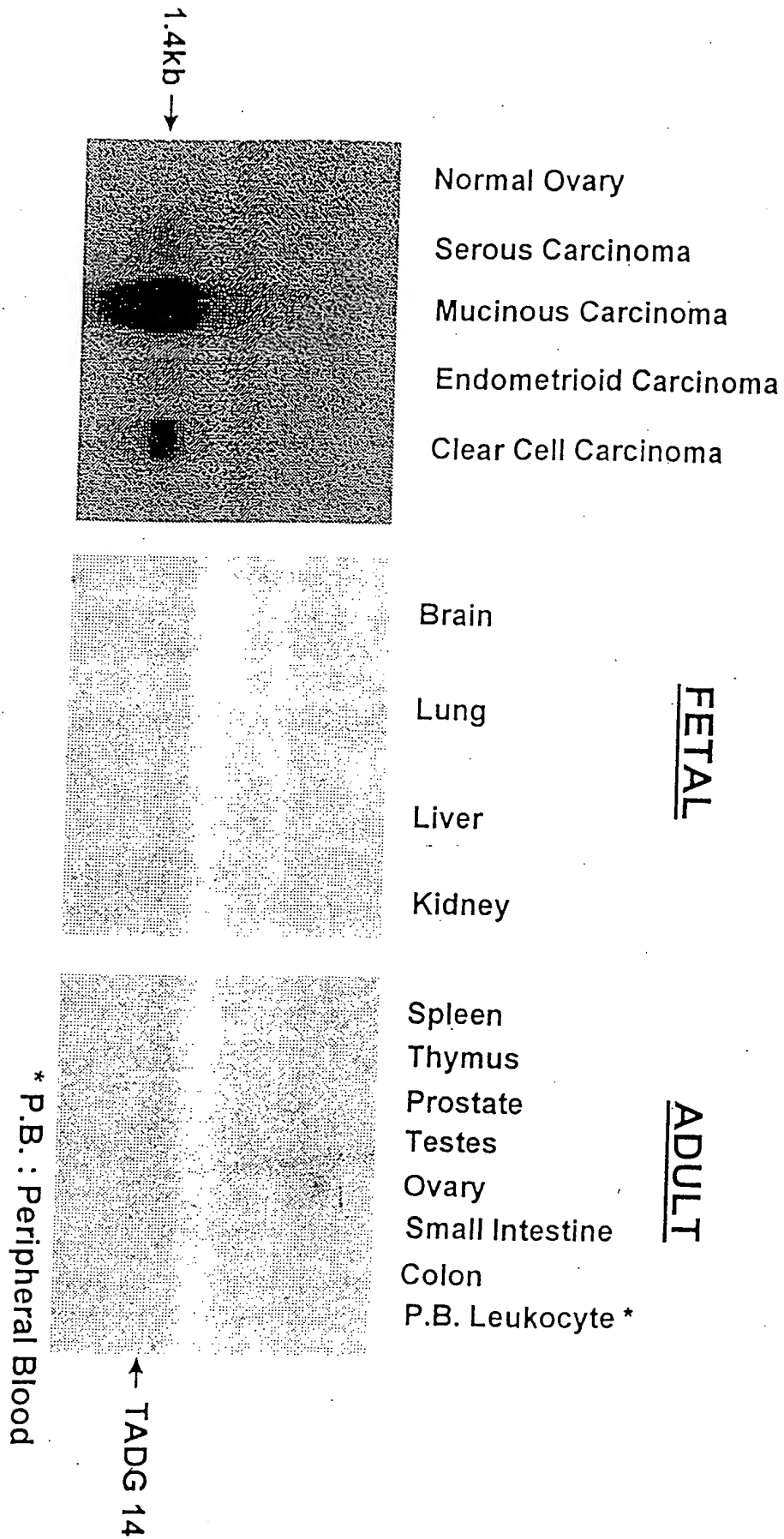


Fig. 5

Replacement Sheet

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1  CTGTAGCAGGCAGAGCTTACCAAGTCTCTCCGAAC TCAAATGGAAGAAATACCTTATGAA 60
61  TGTAAGAATGTAGGGGGTCATGGCTTGTAAATTTACACAGTGTAATGAAACCATCCTAGA 120
121 GGATTATGAGGAATCCTTTCTATGTGATTTTCAATCATAGCAAGCAAGAAAGGCTCCAGT 180
181 GTCAAGGTAGTTCAGCTCTTACAGGATATAAAACAGTCCATACTTGAGAGAAAAAACTTA 240
241 GATCTGAGTGATGGAATGTGAAGCAAATCTTTCAAATCAGTAGACATTTCTTGGACATA 300
301 AAACACAGATGAGGAAAGGGCTTCAAATTAGAAGTTACGTAATCACCATCAGAAAGTTCA 360
361 TGTTTGGTAAATTCTGTTACTAGAAATGTAGGAAATTCAGGTATAGCTTTGAATCCCAAT 420
421 TACACATTGGTCAGTGGGAAAATAAGGGCCTCCAACAGGCAAATTCAGGGAGGATAGGT 480
481 TTCAGGGAATGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGTGCGG 540
                                     M G R P R P R A A -
541 CCAAGACGTGGATGTTCTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCAC 600
      K T W M F L L L L G G A W A G H S R A Q -
601 AGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG 660
      E D K V L G G H E C Q P H S Q P W Q A A -
661 CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCTTGTAGGTGGCAACTGGGTCC 720
      L F Q G Q Q L L C G G V L V G G N W V L -
721 TTACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTAC 780
      T A A H+C K K P K Y T V R L G D H S L Q -
781 AGAATAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCT 840
      N K D G P E Q E I P V V Q S I P H P C Y -
841 ACAACAGCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACC 900
      N S S D V E D H N H D+L M L L Q L R D Q -
901 AGGCATCCCTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTG 960
      A S L G S K V K P I S L A D H C T Q P G -
961 GCCAGAAGTGCACCGTCTCAGGCTGGGGCACTGTCAACAGTCCCCGAGAGAATTTTCCTG 1020
      Q K C T V S G W G T V T S P R E N F P D -
1021 ACACTCTCAACTGTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACC 1080
      T L N C A E V K I F P Q K K C E D A Y P -
1081 CGGGGCAGATCACAGATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCC 1140
      G Q I T D G M V C A G S S K G A D T C Q -
1141 AGGGCGATTCTGGAGGCCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGG 1200
      G D S+ G G P L V C D G A L Q G I T S W G -
1201 GCTCAGACCCCTGTGGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACC 1260
      S D P C G R S D K P G V Y T N I C R Y L -
1261 TGGACTGGATCAAGAAGATCATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCT 1320
      D W I K K I I G S K G * SEQ ID No. 6
1321 CCCTTAATAAACTCACGGAATTC SEQ ID No. 7

```

 = Kozak's Consensus sequence

+ = Conserved amino acids of catalytic triad H, D, S

NSS = Possible N - linked glycosylation site

— = Poly - adenylation signal

 = Conserved nt of catalytic triad

○ = aa required for formation of an oxyanion hole for catalytic activity

FLLL = Secretion signal sequence

Fig. 6

1

T14 SEQ ID No. 9

Fig. 7B


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Tadg14 1 MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAAL 50
      |||| | | . |. ||| ||||| .||| |:| || |||||
Neurop 1 MGRPPPCAIQPWILLLLFMGAWAGLTRAQGSKILEGRECIPHSQPWQAAL 50

      51 FQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPV 100
      |||:|:||||| ||||| |||.|||||:| |||||
      51 FQGERLICGGVLVGDRWVLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQV 100

      101 VQSIPHPCYNSSDVEDHNNHDLMLLQLRDQASLGSKVKPISLADHCTQPGQ 150
      ||| |||||.|. |||.||:|:|.|. |.|| |||: ||. |. ||
      101 AQSIQHPCYNNSPEDHSHDIMLIRLQNSANLGDKVKPVQLANLCPKVGQ 150

      151 KCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAG 200
      || :|||||||.|||||:| ||| |||||.||:|||||
      151 KCIISGWGTVTSPQENFPNTLNCAEVKIYSQNK CERAYPGKITEGMVCAG 200

      201 SSKGADTCQGDSGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLD 250
      || ||||| ||||| ||||| |||||: : ||||| |||||
      201 SSNGADTCQGDSGGPLVCDGMLQGITSWGS DPCGKPEKPGVYTKICRYTT 250

      251 WIKKIIGSKG 260 SEQ ID No. 7
      |||| . .:
      251 WIKKTM DNRD 260 SEQ ID No. 10

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Fig. 8

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